

M A L L A R I L R A G L R P A P E R G G SEQ ID NO:2
 ATG GCC CTG CTG GCG CGG ATC CTG AGA GCC GGG CTG CGG CCG GCG CCC GAG CGG GCT GGG SEQ ID NO:1
 ↑SEQ ID NO:3→
 L L G G G A P R R P Q P A G A R L P A G 40
 CTC CTG GGC GGC GGG GCC CCG CGG CGG CCT CAA CCC GCG GGC GCA CGG CTC CCG GCG GGG 120
 A R A E D K G A G R P G S P P G G G R A 60
 GCG CGG GCC GAG GAC AAA GGC GCC GGG CGG CCG GGG TCG CCG CCG GGA GGG GGC CGA GCC 180
 E G P R S L A A M P G P R T L A N L A E 80
 GAG GGT CCC CGG AGC CTC GCC GCC ATG CCG GGG CCG AGG ACC CTC GCC AAC CTG GCG GAG 240
 F F C R D G F S R I H E I Q Q K H T R E 100
 TTC TTC TGC AGG GAC GGC TTC AGC CGC ATC CAC GAG ATC CAG CAG AAG CAC ACA CGG GAA 300
 Y G K I F K S H F G P Q F V V S I A D R 120
 TAT GGA AAA ATC TTC AAG TCT CAC TTT GGT CCT CAG TTT GTA GTA TCT ATT GCA GAC CGC 360
 D M V A Q V L R A E G A A P Q R A N M E 140
 GAT ATG GTG GCT CAG GTG CTC CGG GCG GAG GGC GCT GCG CCC CAG AGA GCC AAC ATG GAG 420
 S W R E Y R D L R G R A T G L I S A E G 160
 TCC TGG CGG GAG TAC CGA GAC TTG CGG GGG AGA GCC ACC GGG CTC ATC TCG GCG GAG GGT 480
 E Q W L K M R S V L R Q R I L K P K D V 180
 GAA CAG TGG CTC AAG ATG AGA AGC GTA TTG AGA CAA AGA ATT CTG AAA CCG AAA GAT GTG 540
 A I Y S G E V D Q V I A D L I K R I Y L 200
 GCC ATT TAT TCT GGA GAA GTC GAC CAA GTT ATT GCT GAC TTA ATT AAA AGA ATC TAC CTC 600
 L R S Q A E D G E T V T N V N D L F F K 220
 CTC AGG AGC CAG GCA GAA GAT GGA GAA ACC GTG ACC AAT GTC AAT GAT CTT TTC TTC AAA 660
 Y S M E G V A T I L Y E S R L G C L E N 240
 TAT TCA ATG GAA GGA GTG GCC ACC ATC CTT TAT GAG AGT CGT TTG GGC TGC CTG GAA AAC 720
 S I P Q L T V E Y I E A L E L M F S M F 260
 AGC ATC CCA CAG CTG ACT GTG GAA TAC ATC GAG GCC CTG GAG CTC ATG TTT AGC ATG TTC 780
 K T S M Y A G A I P R W L R P F I P K P 280
 AAG ACC TCC ATG TAT GCA GGC GCC ATC CCC AGA TGG CTT CGC CCC TTC ATC CCA AAG CCC 840
 W R E F C R S W D G L F K F S Q I H V D 300
 TGG CGG GAA TTC TGC AGG TCC TGG GAT GGA CTC TTC AAA TTC AGC CAA ATT CAT GTT GAC 900
 N K L W D I Q Y Q M D R G R R V S G G L 320
 AAC AAG TTG TGG GAC ATA CAG TAC CAA ATG GAC CGA GGC CGG AGG GTG AGC GGG GGA CTT 960
 L T Y L F L S Q A L T L Q E I Y A N V T 340
 CTC ACA TAC CTC TTC CTT AGC CAG GCT CTG ACG CTG CAG GAG ATC TAC GCC AAC GTG ACT 1020
 E M L L A G V D T T S F T L S W T V Y L 360
 GAG ATG CTG CTG GCC GGC GTC GAC ACG ACG TCC TTC ACC TTG TCT TGG ACG GTG TAC CTC 1080

FIG. 1a

L A R H P E V Q Q T V Y R E I V K N L G 380
CTG GCA AGG CAC CCA GAA GTG CAG CAG ACG GTG TAC CGG GAG ATT GTG AAG AAT TTA GGG 1140

E R H V P T A A D V P K V P L V R A L L 400
GAA AGG CAT GTT CCA ACT GCA GCT GAT GTC CCC AAG GTC CCG CTG GTC AGA GCT CTC CTT 1200

K E T L R L F P V L P G N G R V T Q E D 420
AAG GAA ACC CTG AGG CTG TTT CCA GTG CTG CCA GGG AAC GGC CGG GTC ACC CAG GAA GAC 1260

L V I G G Y L I P K G T Q L A L C H Y A 440
CTG GTT ATT GGC GGG TAT CTG ATT CCG AAA GGC ACC CAG CTG GCC CTT TGC CAC TAT GCC 1320

T S H Q D E N F P R A K E F R P E R W L 460
ACA TCG CAC CAG GAT GAG AAC TTC CCT CGG GCC AAG GAG TTC CGA CCT GAG CGC TGG CTG 1380

R K G D L D R V D N F G S I P F G H G V 480
CGG AAA GGA GAC TTA GAT AGA GTT GAC AAT TTT GGA TCC ATC CCC TTT GGT CAT GGG GTT 1440

R S C I G R R I A E L E I H L V V I Q L 500
CGC AGC TGC ATA GGG CGG AGA ATT GCA GAA CTG GAG ATT CAC CTC GTC GTG ATC CAG TTG 1500

L Q H F E I K T S S Q T N A V H A K T H 520
CTT CAA CAT TTT GAG ATC AAA ACA TCT TCT CAG ACC AAT GCT GTT CAT GCA AAA ACC CAC 1560

G L L T P G G P I H V R F V N R K * 538
GGG CTC CTG ACG CCA GGG GGG CCC ATC CAC GTG CGA TTT GTT AAC AGA AAG TAA 1614

←SEQ ID NO:3↑

GCCTAGATTTTAAACCTGGGCTGATGTAGCAGACCAGCTCGCCGACACACAGTGGGTATTTGTGTTCGCTGATCACCGT

GGAGAAGGAAAGCGATGTGCGCTAAAGGCTGTCTTGTATAGACTGGCCTCCAGGTCTGGGACACTTGTAATCTTTA

TGCAAAGTAATGTAAAAAGGTTGCTATTTTACTGGTGCATACCAGAAGTTGCCCTTTCTTTGGGGGAAACAGCTGTTTA

AAAACCAGTGGCAGTGAATTTTTATGCTTCATACATTGNGCTAGACTCAATATTTAATGACTGGCAGTATCCTGTGCAT

TTACTTGTACAGGGAAATGGTGGNTTACTTACAAATTCAGTTCTTC

FIG. 1b

09945301-033401

FOIEBO F0E5H660

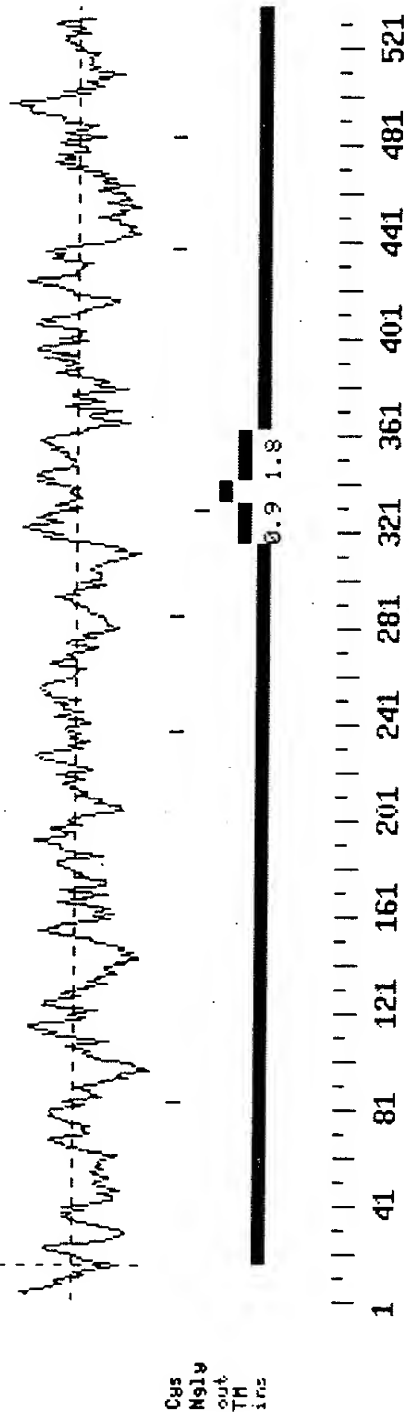


FIG. 2

```

*->PPgPpplPliGnll.qlgrapgppiph.sltklrkakrYGkpvftlyl SEQ ID NO:4
PgP 1 ++ ++ g+ i h++ +k + + YG ++f ++
27439 69 MPGPRTLANLAEFFcRDGF--SRI-HeIQQKHTR-E-YG-KIFKSHF 109

GprpvVvltgpeavkevLidkgeeFakgRgdfnptfpwlskgyre.....
Gp+ vV + + ++v +vL +g ++ R + + w+ yr+ +++
27439 110 GPQFVVSIADRDMVAQVLRAEGAAPQ--RANM---ESWR--EYRDlrgra 152

qglifsdnGpkWrklRrFsltlrfHFgmGaysKrsqkleePriqeeard
+gl+ + +G++W k+R l +r +++ +++++ +++++ d
27439 153 TGLISA-EGEQWLKMRS--VLRQRI-LKP-----KDVAIYSGEVDQVIAD 193

Lverlrk...eqa.gspi.DitellarlaplnvIcsllFGvrfdyr...
L++r+ ++++++g+++++ +l++ ++ ++ ++ +l+ r+++l+++
27439 194 LIKRIYLLrsQAEdGETVtNVNDLFF-KYSMEGVATILYESRLGCLensi 242

peDp.eflklidkllnemfdrvspwhqlldifP.fLlrylpgsfkrkafk
p + e++ +++ l+ mf ++s+ ++ +P++L+++ p++ +r+ +
27439 243 PQLTVEYIEALE-LMFSMF-KTSM--YAG-AIPrWLRPFIPKP-WREFC- 285

aakd.lkdyldklierretlepagdpRrld.i.....gflDslLleakr
+ +d+l+++ + + + ++ + + D+ ++ ++g+l + l++++
27439 286 RSWDgLFKFSQIHVDNKLW--DI-QYQM--DrGrvsgGLL-T-YLFLSQ 328

eggnpkxselsdeelaatvldllfAGteTTsstLswaLylLakhPevqakl
l+ e+ a+v ++l AG++TTs tLsw++ylLa+hPevq+ +
27439 329 -----ALTlQEiYANVTEMLLAGVDTTSTLswTVYLLARHPEVQQTv 371

reEideviGrdrsptydvDaraqmPYLdAvIkEtLRlypvvPlllpRvat
+ Ei +G pt D +++ P++ A +ketLRl+pv+P + +Rv+
27439 372 YREIVKNLGERHVPtAA-D-VPKVPLVRALLKETLRlFPVLP-GNGRVtQ 418

kDteiPdGylIPKGtLVivnlyslhrDpkvfpnPeeFdPeRFL.....de
+D +i +GylIPKGt+ ++ y+ + ++ fp++ eF+PeR+L++++ d
27439 419 EDLVI-GGYLIPKGtQLALCHYATSHQDENFPRAKEFRPERWlRkgdlDR 467

ngkfkkksyafLPFGaGpRnClGerlArmElflfLatlLqrFPelelavpp
+ + +PFG+G+R+C+G+r+A++E+ l++++lLq+F e++++ +
27439 468 ----VDNFGSIPFGHGVRSICGRRIAELIHLVVIQLLQHF-EIKTSSQT 512

gdipsltpkpelglskpplykvqlrpa<-*
++ + + ++l++ +p++ +r +
27439 513 NAVH-AKTH--GLLTPGGPIH---VR-F 533

```

FIG. 3

09945301.083101
 10 FEB 80 10:54:56

Query: 146 RDLRGRATGLISAEGEQWLKMRSVLRQRILKPKDVAIYSGEVDQVIADLIKRIYLLRSQA 205
 RD RG A GL++AEGE+W ++RS L +++KP++V Y ++++V D ++R+ +R Q
 Sbjct: 11 R DYRGEAYGLLTAEGEWQRLRSALNPKLMKPQEVKNYIPKLNEVSQDFVERLRKMRDQG 70 SEQ ID NO:5

Query: 206 E-DGETVTNVNDLFFKYSMEGVATILYESRLGCLN-NSIPQLTVEYIEALELMFSMFKTS 263
 + GE V + + +K++ E + T+L+ RLGCLE N++ ++I+A++ SMF T+
 Sbjct: 71 QGQGELVEDFAEELYKWAFESICTVLFGRKLGCLNENVDPEAQKFIDAVK---SMFHTT 127

Query: 264 MYAGAI PRWL-RPFIPKPWREFCRSWDGLFKFSQIHVDNKLWDIYQMDRG 313
 + +P L R F K W++ R+WD +F Q ++D L ++ + G
 Sbjct: 128 VPMNMMPPELWRYFKTKTKWDHVRWDQIFDVCQKYIDEALERLEKESQSG 178

FIG. 4

Query: 71 GPRTLANLAEFFCRDGFSSRIHE-IQKHTREYKGIFKSHFG-PQFVVSIADRDMVAQVLR 128
 G + L + G + +H+ I +H ++YG IF+ G Q V ++ +++ V +
 Sbjct: 64 GLPVVGTLDLIAAGGATHLHKYIDARH-KQYGPFRERLGGTQDAVFVSSANLMRGV FQ 122 SEQ ID NO:6

Query: 129 AEGAAPQRANMESWREYRDLRGRATGLISAEGEQWLKMRSVLRQRILKPK----DVAIYS 184
 EG PQ ++W Y GL EG +WL R +L + +L DV I S
 Sbjct: 123 HEGQYPQHPLPDWTLNQQHACQGRGLFFMEGAEWLHNRRLNRLLLNGLNLMWMDVHIES 182

Query: 185 GEVDQVIADLIKRIYLLRSQ---AEDGET---VTNVNDLFFKYSMEGVATILY-ESRLG 236
 + + D KR + AE GE + + +++S+E + I++ S L
 Sbjct: 183 --CTRRMVDQWKRRTAEEAAIPLAESGEIRSYELPLLEQQLYRWSIEVLCCIMFGTSVLT 240

Query: 237 CLENSIPQLTVEYIEALELMFSMFKTSMYAGAI PRWL RPFIPKP-WREFCRSWDGLFKFS 295
 C + Q +++Y +++ +F+ S P L + P WR+F + D + +
 Sbjct: 241 CPKI---QSSLDYFT--QIVHKVFEHSSRLMTFPPRLAQILRLPIWRDFEANVDEVLRG 295

Query: 296 QIHVDNKLWDIYQMDRGRVSGGLTYLFLSQALTLQEIYANV-TEMLLAGVDTTSTFTL 354
 +D+ I+ Q D+ R L Y L A ++ + ++++A DTT+F+
 Sbjct: 296 AAIIDHC---IRVQEDQRRPHDEAL--YHRLQAADVPGDMIKRIFVDLVIAAGDTTAFSS 350

Query: 355 SWTVYLLARHPEVQQT VYREIVKNLGERHVPTAADVPKVPLVRALLKETLRLF 407
 W ++ L++ P +QQ + +E N R L+ L+KE+LRL+
 Sbjct: 351 QWALFALSKEPRLQQLAKERATN-DSR-----LMHGLIKESLRLY 390

FIG. 5

Query: 66 LAAMPGPRTLANLAEFFCRDGFSSRIHEIQKHTREYKGIFKSHFGPQFVVSIADRDMVAQ 125
 LA +PGP TL L + FC+ +HE+Q YG ++ S FG Q V++A +V Q
 Sbjct: 37 LADIPGPGTLRFLFQLFCKGYLLHLHELQVLGKARYGPMWMSFSGTQRTVNLASPPLVEQ 96 SEQ ID NO:7

Query: 126 VLRAEGAAPQRANMESWREYRDLRGRA 152
 V+R EG P R + E W+E+R RA
 Sbjct: 97 VMRQEGKYPVRCSFEPWKEHRRRHQRA 123

FIG 6

FIG. 4

Query: 389 DVPKVPLVRALLKETLRLFPVLPNGRVTQEDL----VIGG-YLIPKGTQLALCHYATSH 443
D+ K+P + A++KETLRL P +P R ++D+ +GG Y IPKGTQ+ + Y +H
Sbjct: 8 DLQKLPYLDVAVIKETLRLHPPVPTVMRKVKKDMEVSGTVGGEYTIPKGTQVMVSPYVMTH 67 SEQ ID NO:8

Query: 444 QD-ENFPRAKEFRPERWLRKGD 464
+D E +P +EF PERWL +
Sbjct: 68 RDPEYYPDPEEFNPERWLEPSE 89

FIG. 7

Query: 99 REYGKIFKSHFGPQFVVSIAADRMVAQV-LRAEGAAPQRANMESWREYRDLRGRATGLIS 157
++YG IF+ G Q ++ IA+ ++ +V ++ P R+ + S L + GL
Sbjct: 74 KQYGPIFRFQMGRQPLIIIAEALCREVGIKKFKDLPNRS-IPSPISASPLHKK--GLFF 130 SEQ ID NO:9

Query: 158 AEGEQWLKMRSVLRQRILKPKDVAIYSGEVDQVIADLIKRIYLLRSQAEDGETVTNVNDL 217
++W KMR+ + + +P + + + + + + L S+ D ++L
Sbjct: 131 TRDKRWSKMRNTILS-LYQPSHL---TSLIPTMHSFITSATHNLDSPRD---IVFSNL 182

Query: 218 FFKYSMEGVATILYESRLGCLENSIPQLTVEYIEAL-ELMFSMFKTSM-YAGAIP---RW 272
F K + + + + G L P VE + + + ++S + M +G++
Sbjct: 183 FLKLTDDIIGQAAFGVDFG-LSGKKPIKDVEVTDFINQHVYSTQLKMDLSGSLSIILGL 241

Query: 273 LRPFIPKPWREFCRSWDGLFKF---SQIHVDNKLWDIQYQMDRGRRV-SGGLLTYL--- 324
L P + +P+R+ + G + + + +L +I + + S L+ +
Sbjct: 242 LIPILQEPFRQVLKRIPTMDWRVEKTNARLSGQLNEIVSKRAKEAETDSKDFLSLILKA 301

Query: 325 -----FLSQALTLOEIYANVTEMLLAGVDTTSTFTLSWTVYLLARHPEVQQTIVYREIVKNL 379
F T I A E LLAG TT+FTLS +YL++ H +V++ + +EI
Sbjct: 302 RESDPFAKNIFTSDYISAVTYEHLLAGSATTFTLSSVLVYLVSGHLDVEKRLLQEI-DGF 360

Query: 380 GERH-VPTAADVP-KVPLVRALLKETLRLFPV 409
G R +PTA D+ K P + ++KE +R + V
Sbjct: 361 GNRDLIPTAHDLQHKFPYLDQVIKEAMRFYMV 392

FIG. 8

Query: 68 AMPGPRT---LANLAEFFCRDG-FS--RIHEIQQKHTREYGKIFKSHFGP-QFVVSIAADR 120
A+PGPR + NL + G +S R+H+ Q +YG I + P Q +V + D
Sbjct: 23 AIPGPRGPFPGMGNLYNLPGIGSYSWLRHLQAGQDKYKYGAIVRETIVPGQDIVWLYDP 82 SEQ ID NO:10

Query: 121 DMVAQVLRAGAAPQRANMESWREYRDLRG---RATGLISAEGEQWLKMRSVLRQRILKP 177
+A +L E PQR + + +YR R + TGL+ G +W ++R+ +++ + P
Sbjct: 83 KDIALLLN-ERDCPQRRSHLALAQYRKS RPDVYKTTGLLPNGPEWWRI RAQVQKELSAP 141

Query: 178 KDVAIYSGEVDQVIADLIK 196
K V + +VD V + I+
Sbjct: 142 KSVRNFRVQVDGVTKEFIR 160

FIG. 9

0945301-03101
T03E01-03101

Query: 88 SRIHEIQQKHTREYGKIFKSHFGPQFVVSIA DRDMVAQVLR AEGAAPQRANMESWREYRD 147
 + + + + + + + E K FG + + + + + + AQ + + E + N + Y
 Sbjct: 52 TELYDLYIRESMEKYGAVKFFFGSRWNILVSRSEYLAQIFKDEDTFAKSGNQKKI-PYSA 110 SEQ ID
 NO:11

Query: 148 LRGRATG--LISAEGEQWLKMRSVLRQRILKPKDVAIYSGEVDQVIADLIKRIYLLRSQA 205
 L TG +ISA G W R+ + + D I+ + + + LIK L
 Sbjct: 111 LAAY-TGDNVISAYGAVWRNRYRNAVINGLQHFD DAPIFKNA--KILCTLIKNRLL----- 162

Query: 206 EDGETVTNVNDLFFKYSMEGVATILYESRLGCLENSIPQLTVEYIEALELMFS-MFKTSM 264
 +G+T + L + + + + + + G L + I + +F F T
 Sbjct: 163 -EGQTSIPMGPLSQRMALDNISQVALGFDGALTHEKNAFHEHLIRIKKQIFHPFFLTFP 221

Query: 265 YAGAIPRWLRPFIPKPPWREFCRSWDGLFKFSQIHVDNKLWDIQYQMDRGRVSGGLLTYL 324
 + +P P K + + + + L K Q + N Y+ + + + L+
 Sbjct: 222 FLDVLP I---PSRKKAFKDVVSFREL LVKRVQDEL VNN-----YKFEQTTFAASDLIR-A 272

Query: 325 FLSQALTLQEIYANVTEMLLAGVDTTSTFTLSWTYLLARHPEVQQTVYREIVKNLGERHV 384
 + + + + + N+ +L+AG + + +YLLA++ Q R+ V + +
 Sbjct: 273 HNNEIIDYKQLTDNIVIIILVAGHENPQLLFNSSLYLLAKYSNEWQEKL RKEVNGITD-- 329

Query: 385 PTAADV PKVPLVRALLKETLRLFPVL 410
 P + +PL+ A L E +R++P L
 Sbjct: 330 PKG--LADLPLLNAFLFEVVRMY PPL 353

FIG. 10

Query: 396 VRALLKETLRLFPVLPNGRVTQEDLVIGGYLIPKGTQLALCHYATSHQDENFPRAKEFR 455
 +R + ET+RL + P R + + + + GY IP T + + +
 Sbjct: 23 LRQVQDETIRLSTLAPWAARYSDKKVTVCGYTIPAKTPMIHALGVGLKNKTVWENTDSWD 82 SEQ ID
 NO:12

Query: 456 PERWLRKGDLD RVDNFGSIPFG-HGVRSCIGRRIAELEIHLVVIQLLQHFEIKTSSQTNA 514
 P+R+ G R ++F PFG H R C G + E+ + LL FEI
 Sbjct: 83 PDRFSPNGR--RGNDF--CPFGVHSRRKCPGYLFSYFEVGVFASILLSRFEIVPVEGQTV 138

Query: 515 VHAKTHGLLT-PGGPIHVR FVN RK 537
 + + HGL+T P I + +RK
 Sbjct: 139 I--QVHGLVTEPKDDIKIYIRS R K 160

FIG. 11

0945301-053101

Query: 344 LAGVDTTSFTLSWTVYLLARHPEVQQTIVYREIVKNLGERHVPTAADVPKVPLVRALLKET 403
+AG+DT + +L++ +Y + H E + E L PTA + + PL+ + ET
Sbjct: 247 IAGMDTAANSLAFVLYRMHLHSEFLPALRAE-ADALFRDGPPTAEALGRSPLLHRFVMET 305 SEQ ID
NO:13
Query: 404 LRLFPVLP 411
LR+ P+ P
Sbjct: 306 LRVHPIAP 313

FIG. 12a

Query: 69 MPGPRTLANLAEFFCRDGFSSRIHEIQKHTREYKGKIFKSHFGPQFVVSIADRDMVAQVLR 128
+P P L + AE G ++ + + YG +F+ Q + +A + ++
Sbjct: 2 VPAPPFLGHAAEM----GTIKLRPFLTRCYQAYGPVFQLTVPQKITVLAGPEANLFAMK 57 SEQ ID
NO:14
Query: 129 AEGAAPQRANMESWREYRDLRGRATGLISAEGEWLKMRSV 169
EG R+ +E+WR+ G +IS +G + R V
Sbjct: 58 -EGHRVLRS-LEAWRDNDHEMGSDRSMISLDGAEHRAVRRV 96

FIG. 12b

Query: 153 TGLISAEGEWLKMRSVLRQRILKPKDVAIYSGEVDQVIADLIKRIYLLRSQAEDGE--- 209
T IS GEQW KMR V+ I+ PK + G+ + +L+ ++ + ++E
Sbjct: 2 TVAISPYGEQWKMRKVITTEIMSPKRLNWLGLKRTTEADNLVAYVHNMCKSETNNKHG 61 SEQ ID
NO:15
Query: 210 TVTNVNDLFFKYSMEGVATILYESR-LG----CLENSIP-QLTVEYIEALELMFSMFKTS 263
V +V D+ Y V +++ R G ++ P E+++A+
Sbjct: 62 AVIDVRDVVRHYCHNVMMFGRRHFGKGTZFSDDGGPGPEEKEHMDAIFTALDCLYAF 121
Query: 264 MYAGAIPRWLR 274
+ IPRWLR
Sbjct: 122 CVSDYIPRWLR 132

FIG. 13a

Query: 458 RWLRKGDLD 466
RWLR DLD
Sbjct: 129 RWLRGWDL 137 SEQ ID NO:16

FIG. 13b

TOE301-0831060